Big Idea 1: The process of evolution drives the diversity and unity of life.

Enduring understanding 1.A: Change in the genetic makeup of a population over time is evolution.

Essential knowledge 1.A.4: Biological Evolution is supported by scientific evidence from many different disciplines, including mathematics.

a. Scientific evidence of biological evolution uses information from geographical, geological, physical, chemical and mathematical applications.

Evidence for Evolution

- **What does/can the theory of evolution explain?**
- **What observations does/can the theory of evolution support?**
  - **Pesticide Resistance**
  - **Fossil Record**
  - **Biogeography**
  - **Anatomical Observations**
  - **Chemical Analysis / Comparisons**

Essential knowledge 1.A.4: Biological Evolution is supported by scientific evidence from many different disciplines, including mathematics.

b. Molecular, morphological and genetic information of existing and extinct organisms add to our understanding of evolution.

Evidence of student learning is a demonstrated understanding of each of the following:

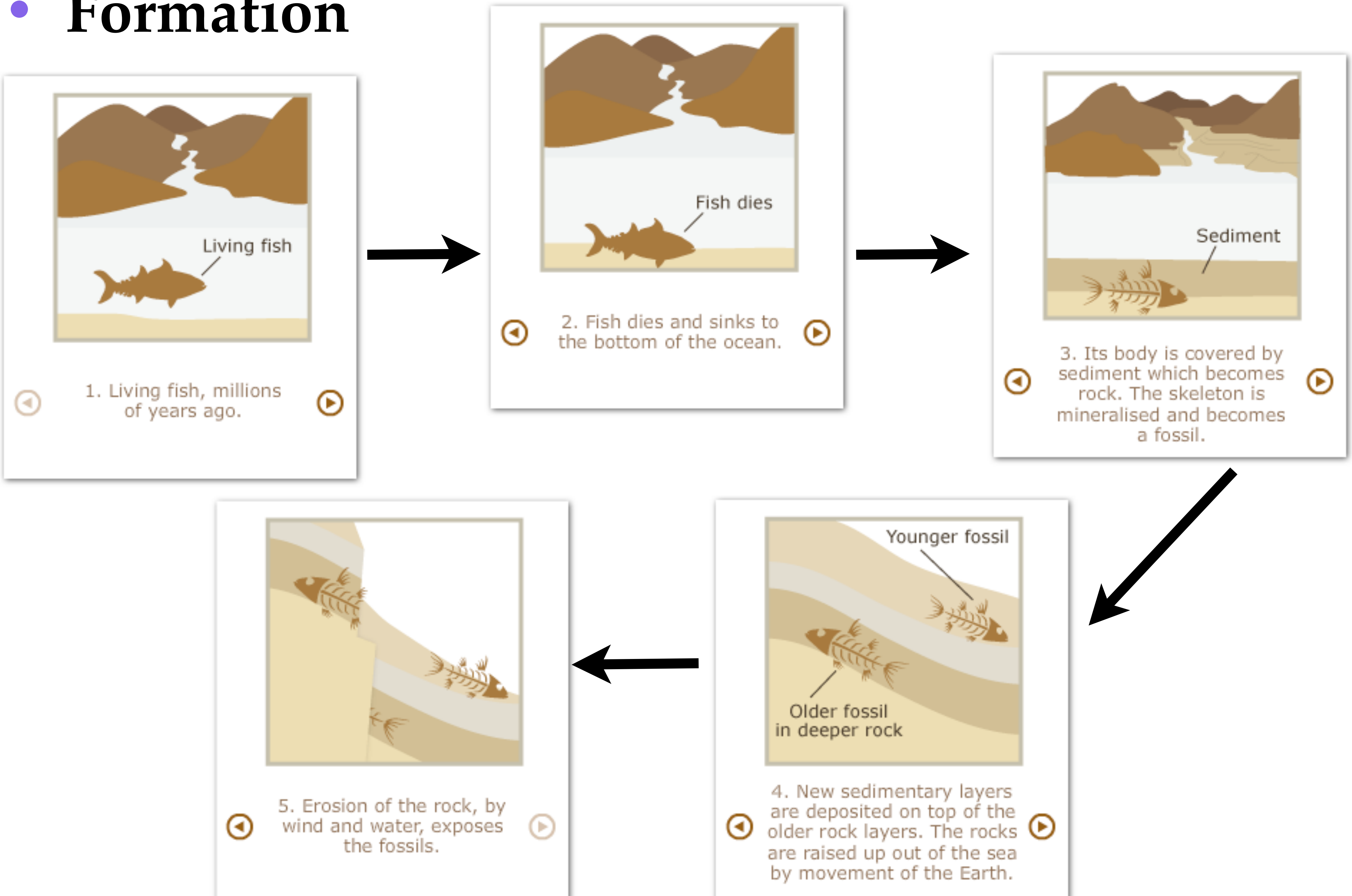
Essential knowledge 1.A.4: Biological Evolution is supported by scientific evidence from many different disciplines, including mathematics.

1. Fossils can be dated by a variety of methods that provide evidence for evolution. These include the age of the rocks where a fossil is found, the rate of decay of isotopes including carbon-14, the relationships within phylogenetic trees, and the mathematical calculations that take into account information from chemical properties and/or geographical data.

✘✘ *The details of these methods are beyond the scope of this course and the AP Exam.*

Fossils

- **Formation**

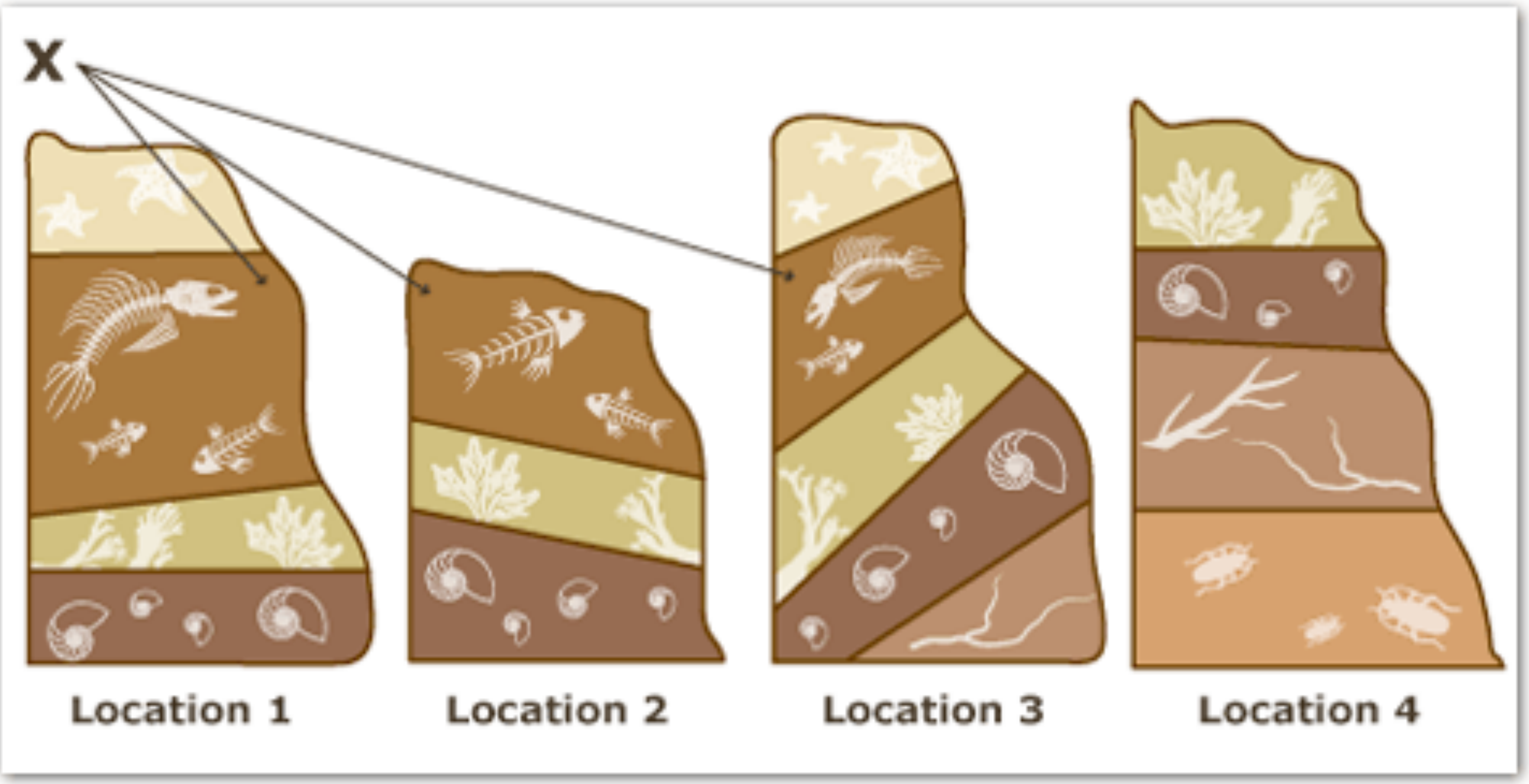


Fossil Record

- **Law of Superposition**

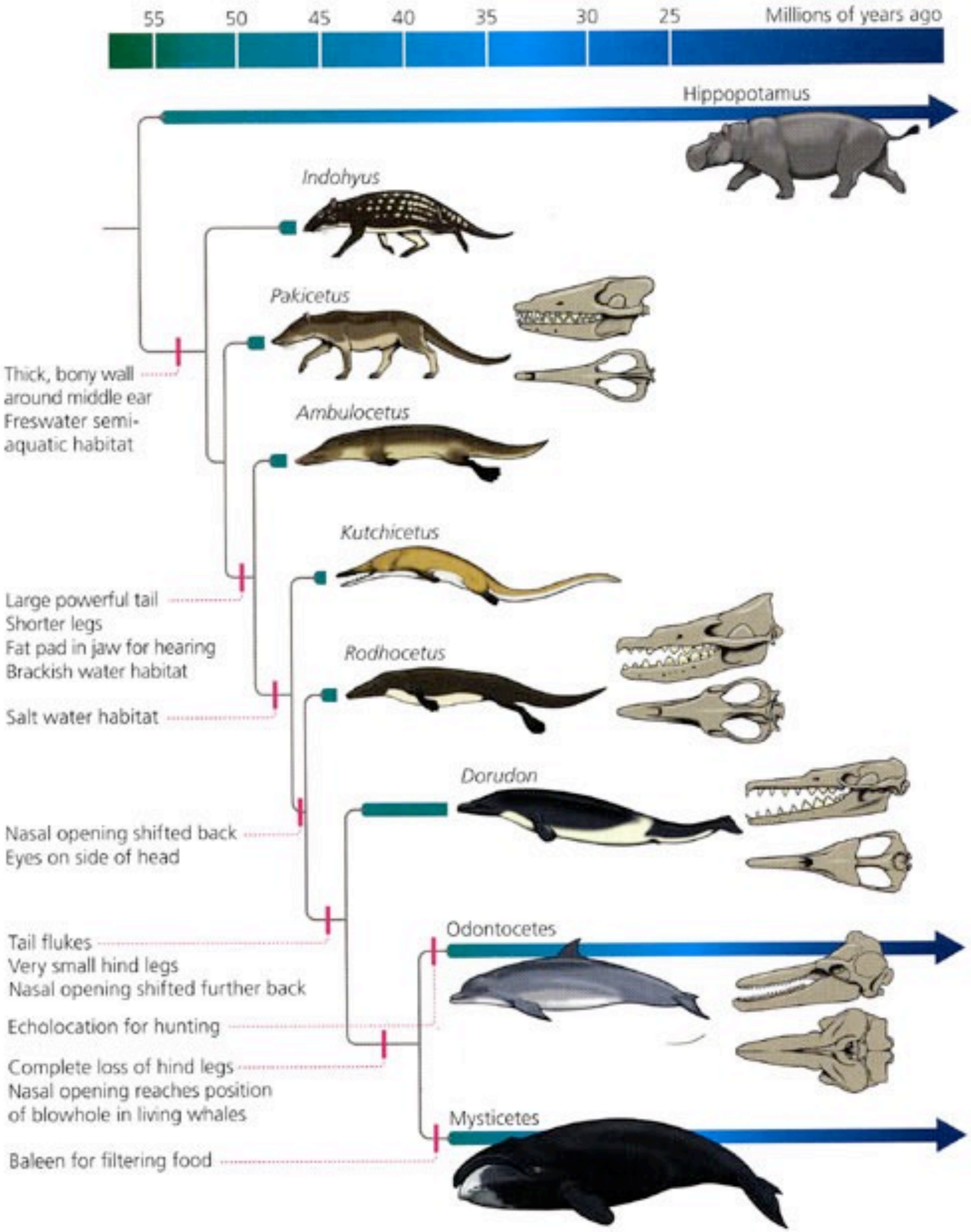
- The lower the strata the older the rock

- **General Pattern**

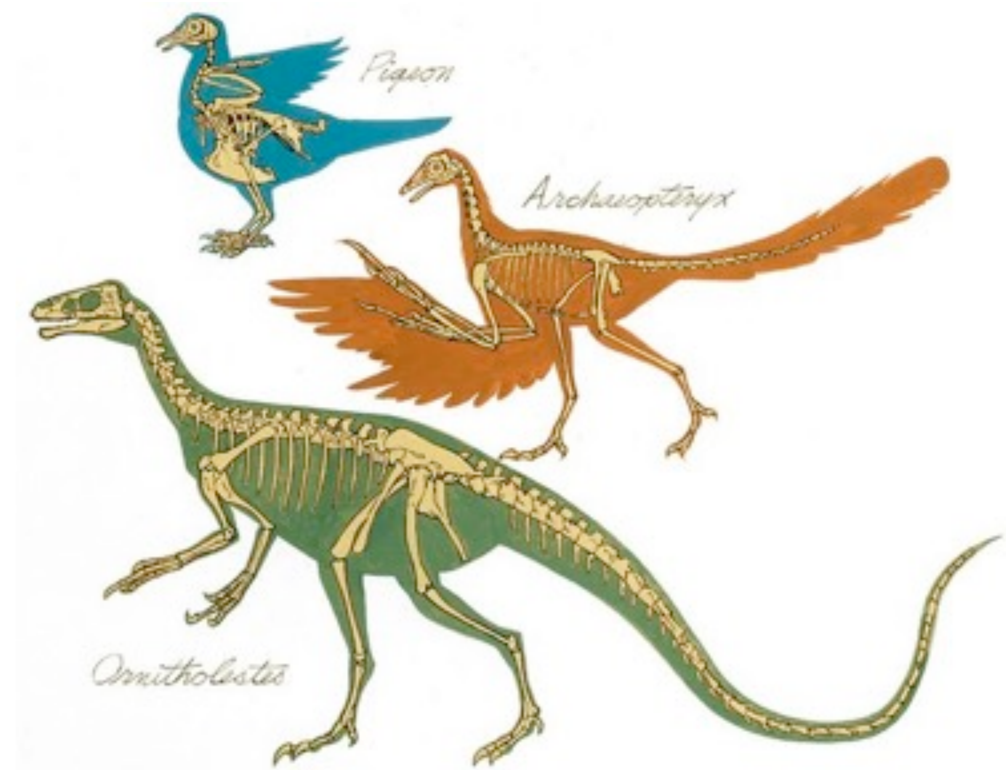


- Shows a succession of forms
- Similar fossils in similar strata
- Older Strata, simpler organisms
- Newer Strata, more complex organisms

Fossil Record



- **Transitional Forms**



Essential knowledge 1.A.4: Biological Evolution is supported by scientific evidence from many different disciplines, including mathematics.

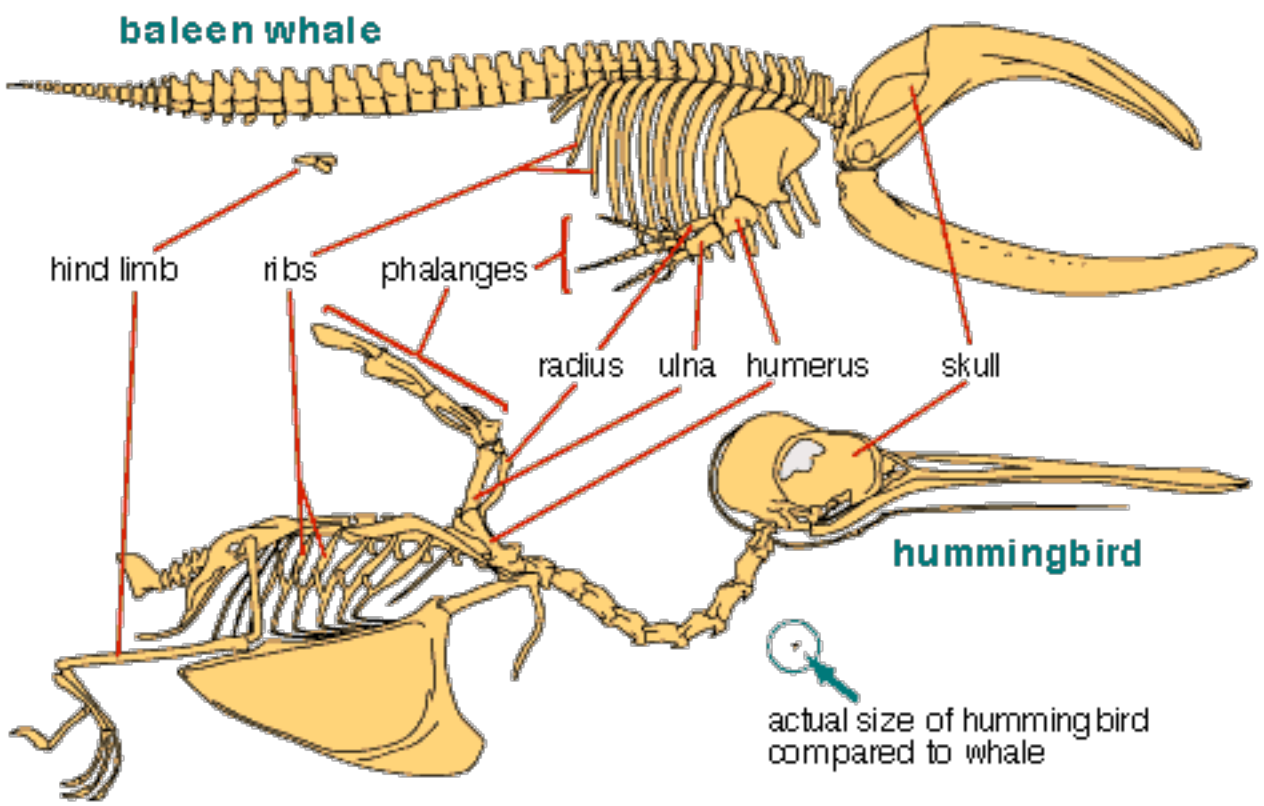
2. Morphological homologies represent features shared by common ancestry. Vestigial structures are remnants of functional structures, which can be compared to fossils and provide evidence for evolution.

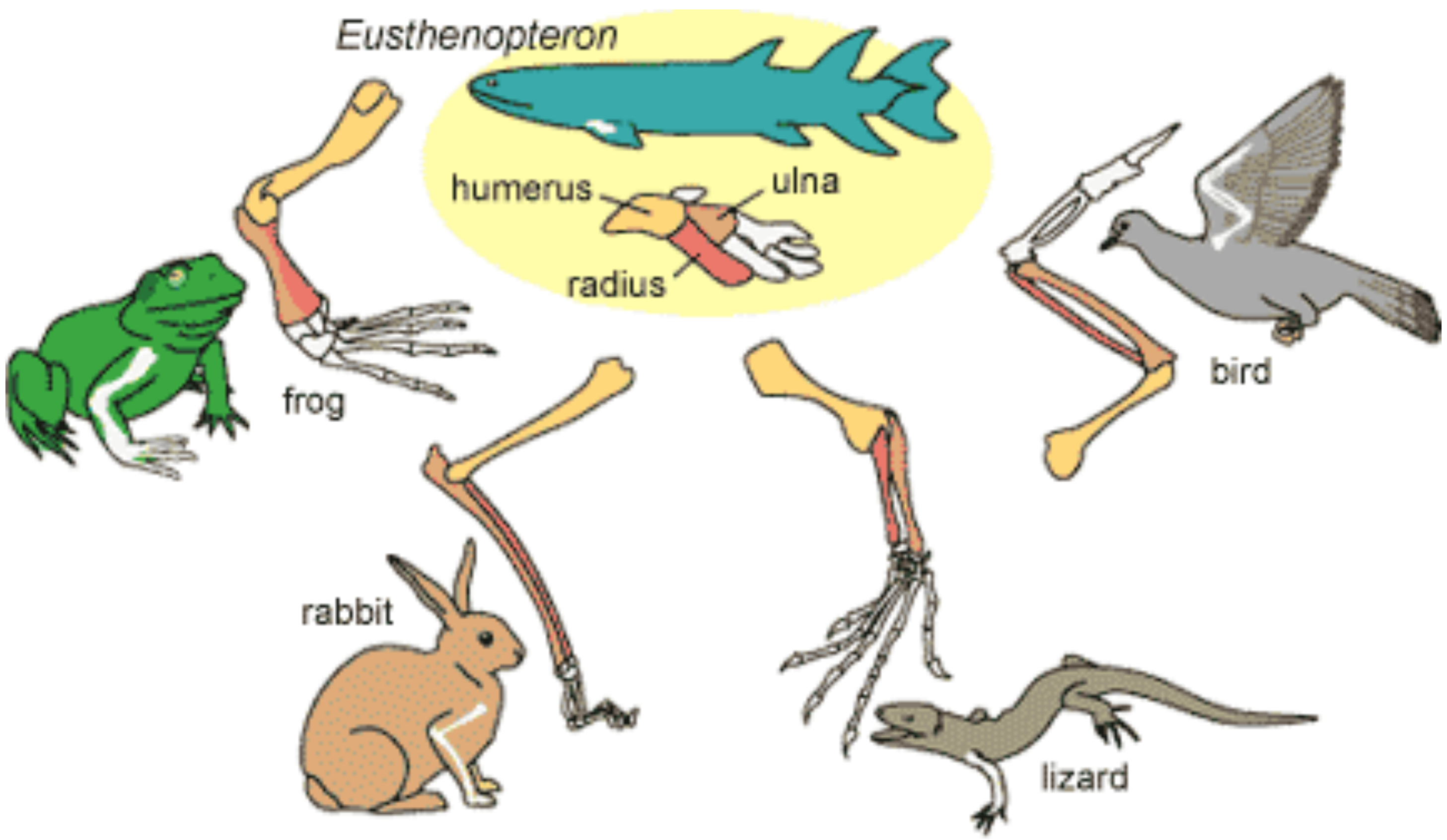
Homology

- **Homology- when related organisms will share certain traits due to common ancestry**
- ***(of course differences in traits are due to divergence as each species adapts to its own environment/challenges)***
    - **Anatomical**
        - **Vestigial Structures**
    - **Embryological**
    - **Cellular**

Anatomical Homology

Although each skeleton appears very different nearly every bone in each has an equivalent in the other



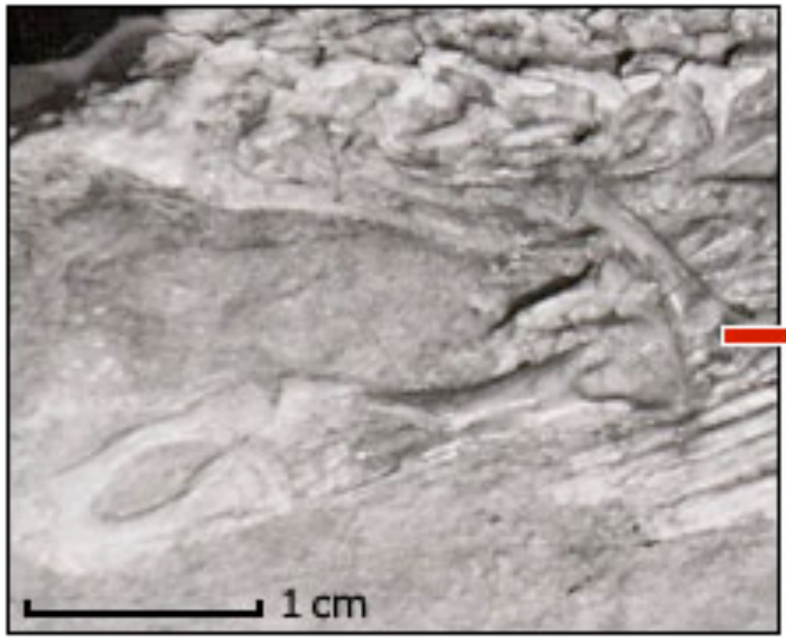


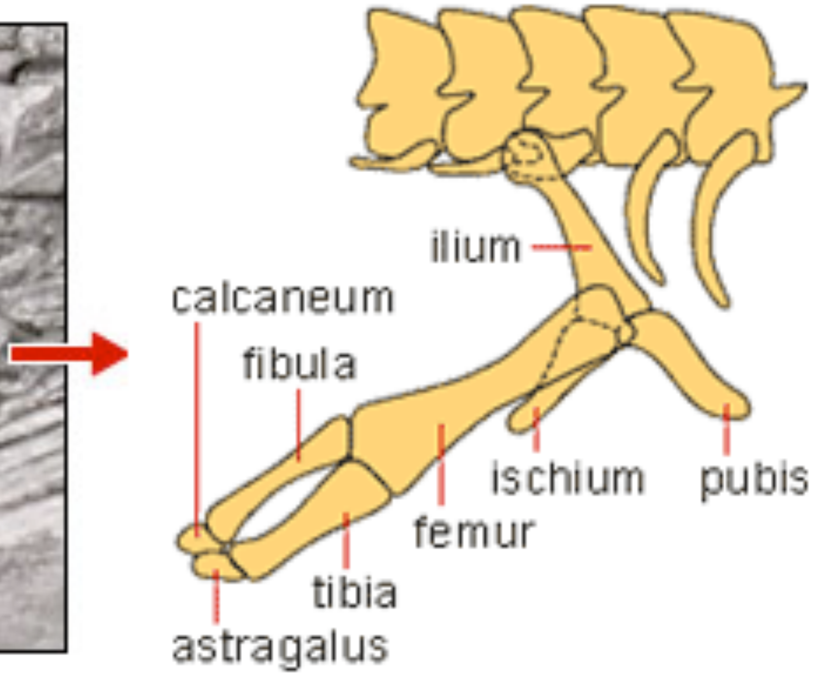
Classic example of tetrapod forelimbs, similar structures, dissimilar functions

Embryological Homology

Snakes have legged ancestors.

Some species of living snakes have hind limb-buds as early embryos but rapidly lose the buds and develop into legless adults. The study of developmental stages of snakes, combined with fossil evidence of snakes with hind limbs, supports the hypothesis that snakes evolved from a limbed ancestor.



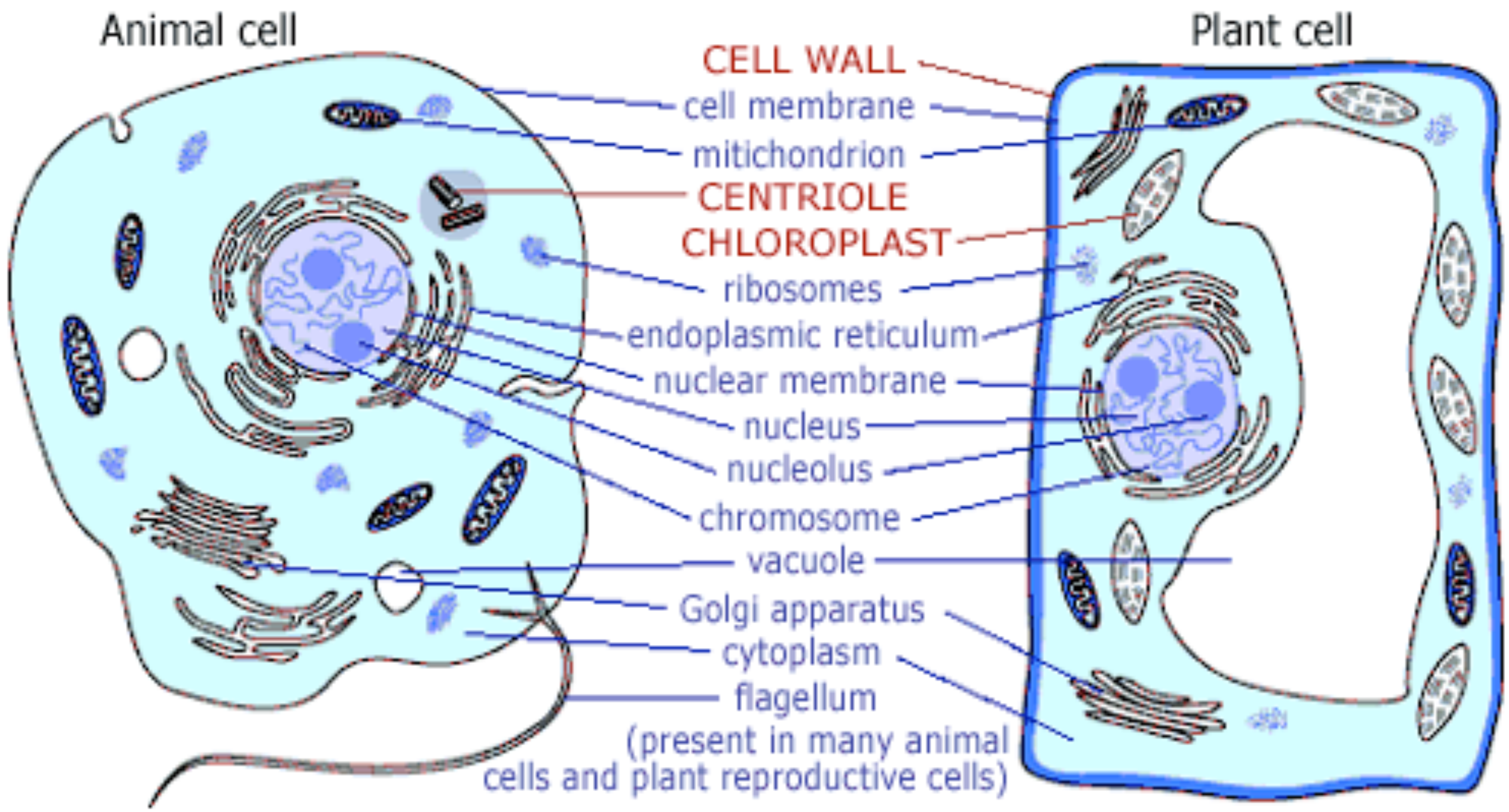


Above left, the Cretaceous snake *Pachyrhachis problematicus* clearly had small hindlimbs. The drawing at right shows a reconstruction of the pelvis and hindlimb of *Pachyrhachis*.

Cellular Homology

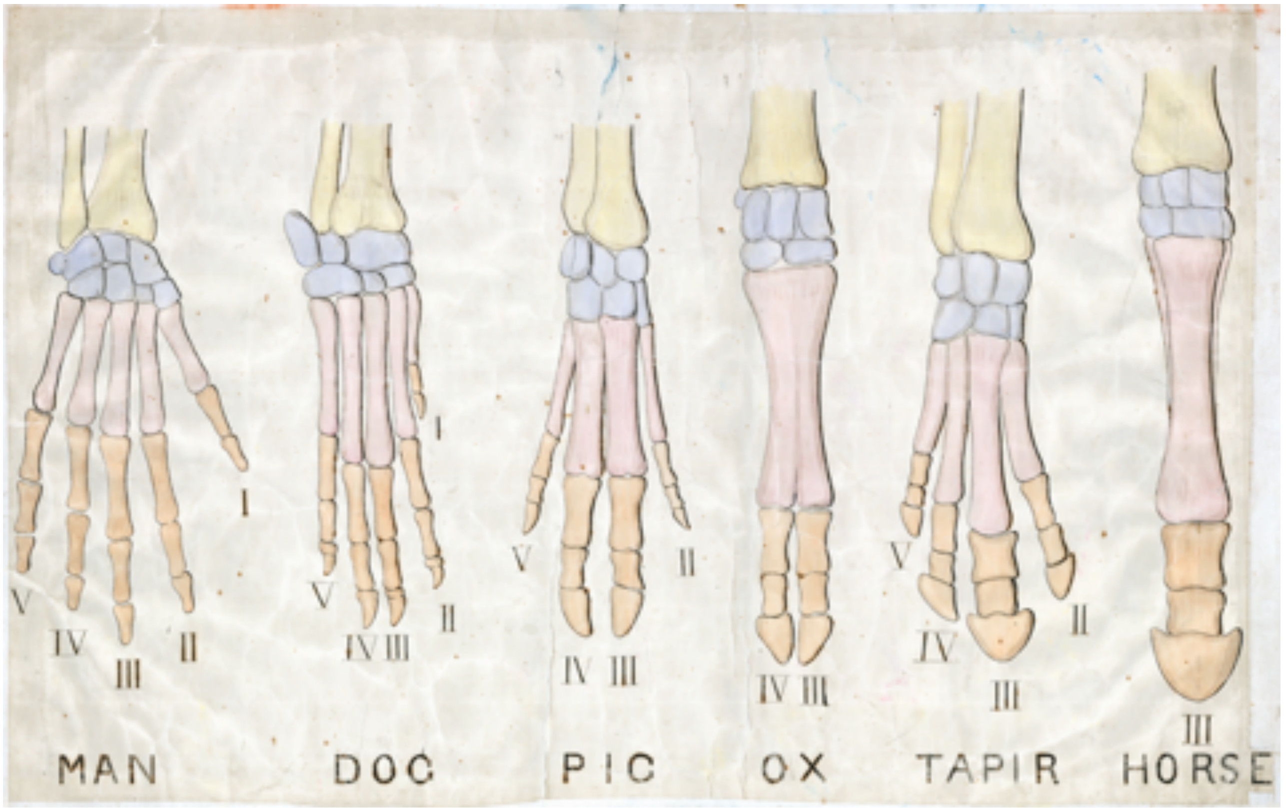
The cellular level

All organisms are made of cells, which consist of membranes filled with water containing genetic material, proteins, lipids, carbohydrates, salts and other substances. The cells of most living things use sugar for fuel while producing proteins as building blocks and messengers. Notice the similarity between the typical animal and plant cells pictured below — only three structures are unique to one or the other.



Vestigial Structures

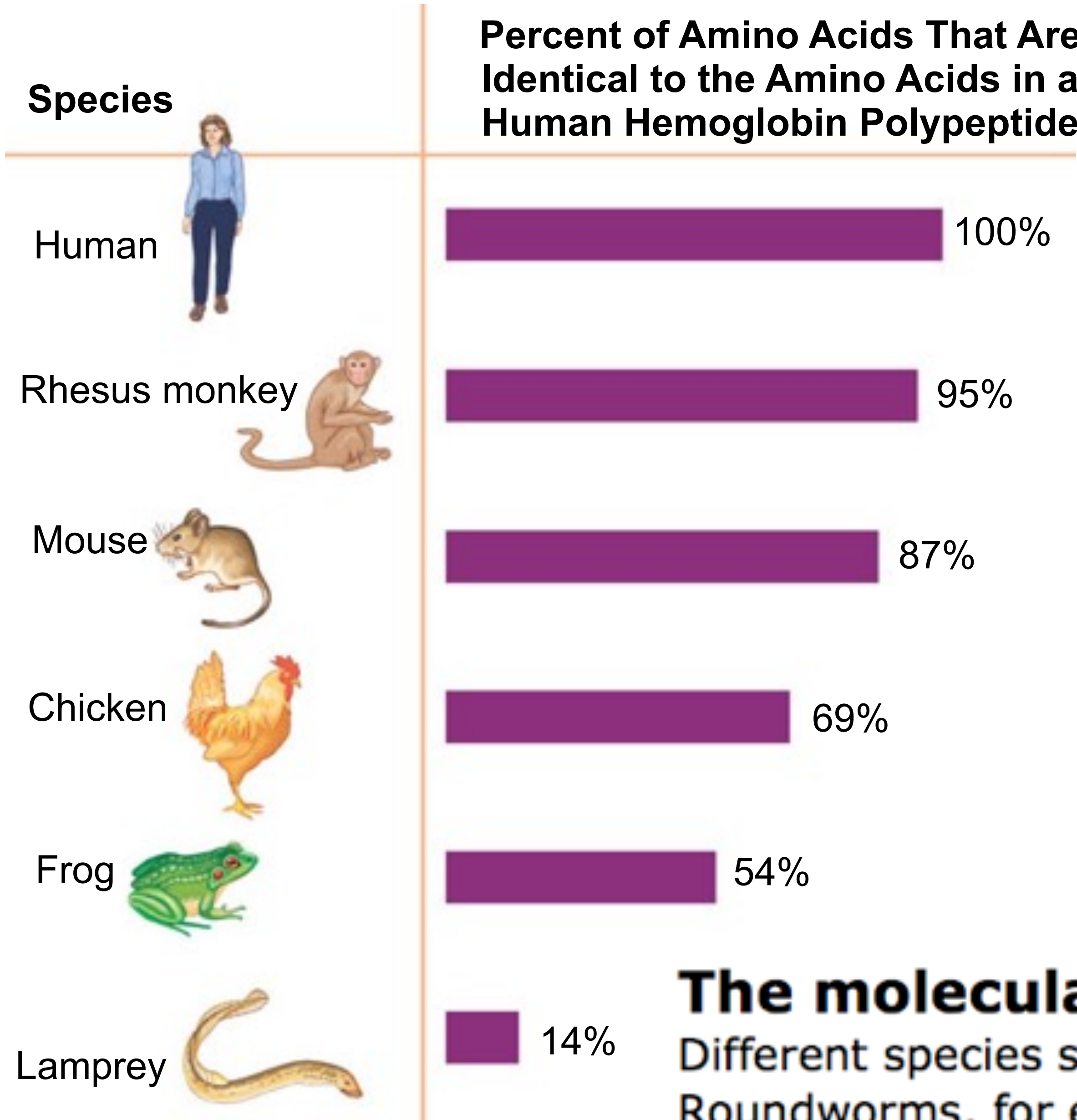
Structures inherited that over time become less functional



Essential knowledge 1.A.4: Biological Evolution is supported by scientific evidence from many different disciplines, including mathematics.

3. Biochemical and genetic similarities, in particular DNA nucleotide and protein sequences, provide evidence for evolution and ancestry.

Molecular Homology



Biologists find homologies in amino acid sequences and nucleotide sequences of both DNA and RNA

The molecular level

Different species share genetic homologies as well as anatomical ones. Roundworms, for example, share 25% of their genes with humans. These genes are slightly different in each species, but their striking similarites nevertheless reveal their common ancestry. In fact, the DNA code itself is a homology that links all life on Earth to a common ancestor. DNA and RNA possess a simple four-base code that provides the recipe for all living things. In some cases, if we were to transfer genetic material from the cell of one living thing to the cell of another, the recipient would follow the new instructions as if they were its own.

Essential knowledge 1.A.4: Biological Evolution is supported by scientific evidence from many different disciplines, including mathematics.

4. Mathematical models and simulations can be used to illustrate and support evolutionary concepts.

To foster student understanding of this concept, instructors can choose an illustrative example such as:

- Graphical analyses of allele frequencies in a population
- Analysis of sequence data sets
- Analysis of phylogenetic trees
- Construction of phylogenetic trees based on sequence data

- Graphical analyses of allele frequencies in a population

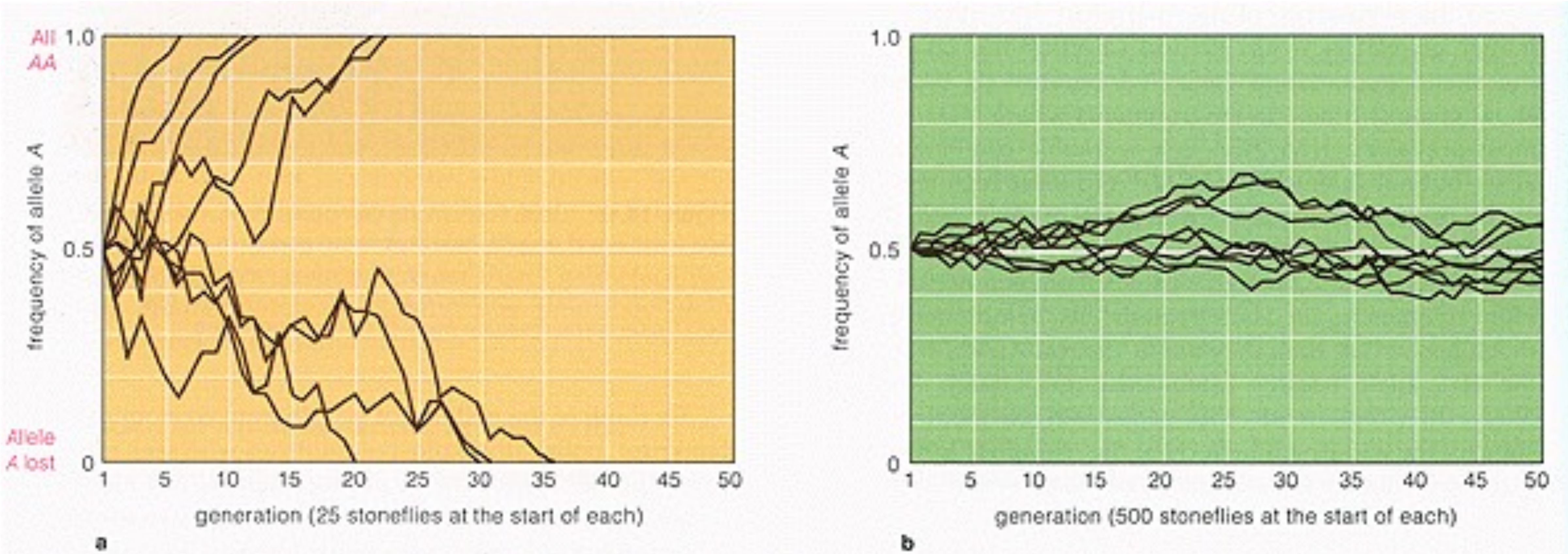


Figure 14.19 Computer simulations of the effect of genetic drift on an allele's frequency in small and large populations. In nine groups of stoneflies, population size was maintained at 25 breeding individuals every generation, for fifty generations. Population size of nine more groups was maintained at 500 for fifty generations. (**a**) Allele *A* became fixed in five of the small populations (the lines reaching the top of the graph) and was lost from four of them (the lines plummeting off the bottom of the graph). As this tells you, even the "best" allele doesn't always win. (**b**) The allele did not become fixed in any large population. Thus the magnitude of drift was much less in every generation than in the small populations.

Equal fitnesses assumed for these simulations:

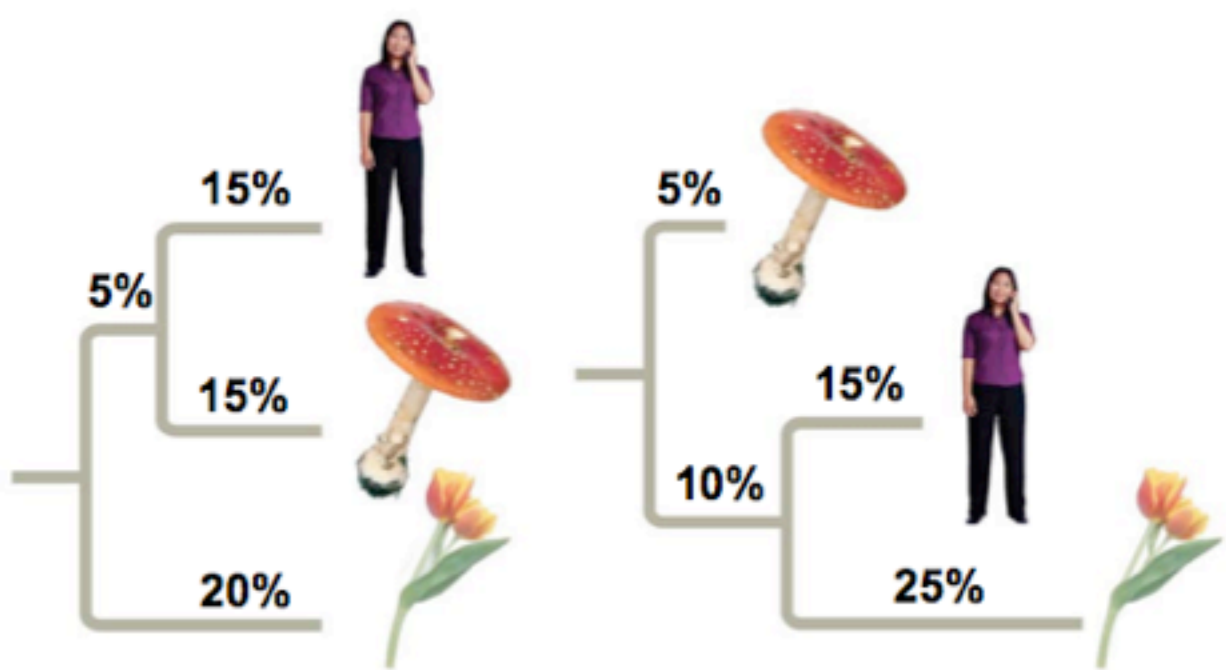
AA = 1
Aa = 1
aa = 1

- Construction of phylogenetic trees based on sequence data

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences

So how do we get here?



Tree 1: More likely   Tree 2: Less likely

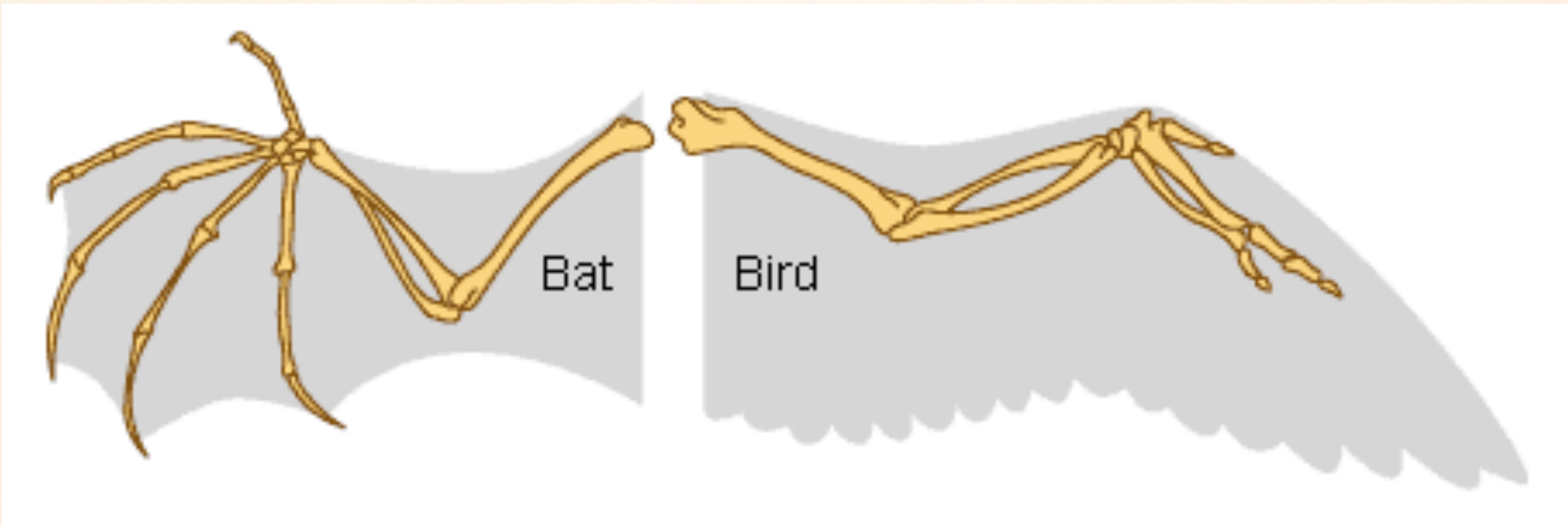
(b) Comparison of possible trees

The answer starts here....

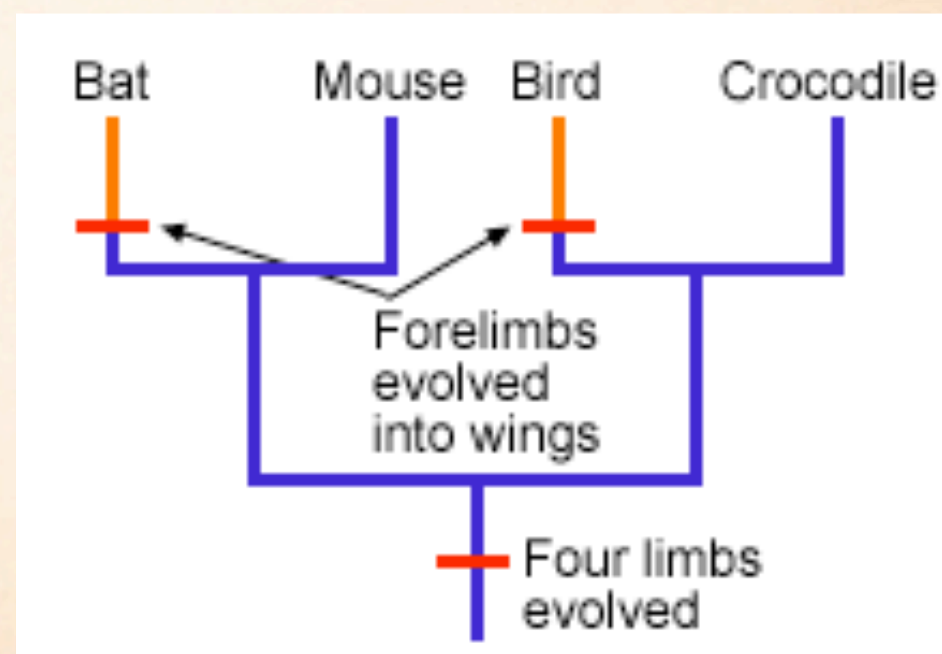
Sorting Homology from Analogy

- One major obstacle in generating phylogenetic trees is distinguishing between homology and analogy.
- Recall Analogy results when organisms are similar due to convergent evolution not because of recent shared ancestry.
- Recall Convergent Evolution occurs when similar environmental pressures and natural selection produce similar adaptations in organisms from different lineages.

- Analogous structures that arose independently are also called **homoplasies**.



- The bat wing consists of stretched skin while the bird uses feathers for flight.
- Ironically birds are more related to crocodiles than bats.



Sorting Homology from Analogy

- Another clue in distinguishing between homology and analogy lies in the complexity of the characters being compared.
- The more elements that are similar in a two complex structures the more likely share a recent common ancestor
- The same argument can be made at the level of the gene.

Evaluating Molecular Homologies

- Comparing DNA sequences between organisms is likely the best way to establish relatedness but its also poses the greatest technological challenges as well.

- To start with DNA in each organism has to be sequenced (challenging by itself but science is better at sequencing everyday and to date has sequenced over 100 billion bases from 1000's of species.

- Next these sequences must be compared (perhaps even more challenging)

- In general, the more the sequences align the more similar they are

Species 1 | Species 2

..ATACGGATACGG..

..TTACGGATACGG..

..**A**TACGGATACGG..
..**T**TACGGATACGG..

Sequence looks similar, difference is likely due to a single base substitution

BUT... What if the single adenine was lost by a deletion mutation? Could it change our interpretation?

Species 1

Species 2

..ATACGGATACGG..

..TTACGGATACGG..

..**T**ACGGATACG**G**_..

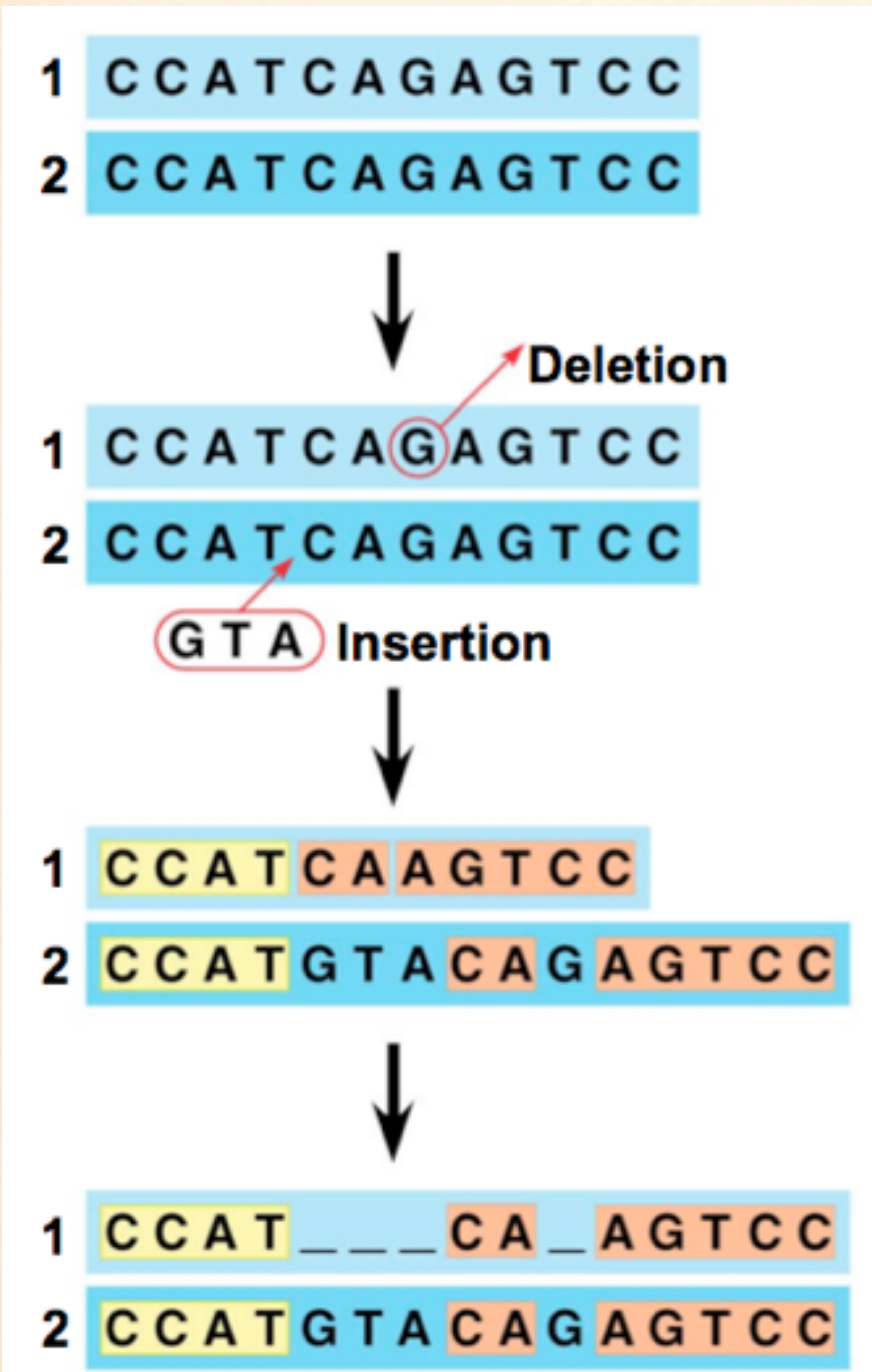
..**T**TACGGATAC**G**G..

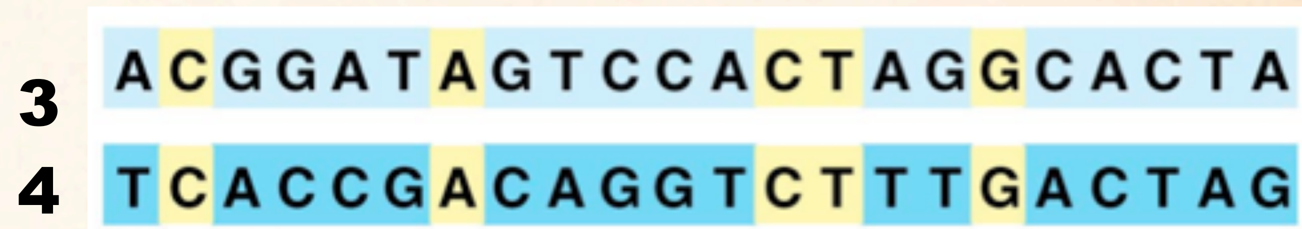
Now the sequence looks very different, when in fact only a single base deletion represents the difference

To address such problems researchers have developed computer programs and statistical tools that estimate the best way to align comparable DNA segments of differing lengths and differentiate among molecular homoplasies.

Species 1
Species 2

Species 3
Species 4

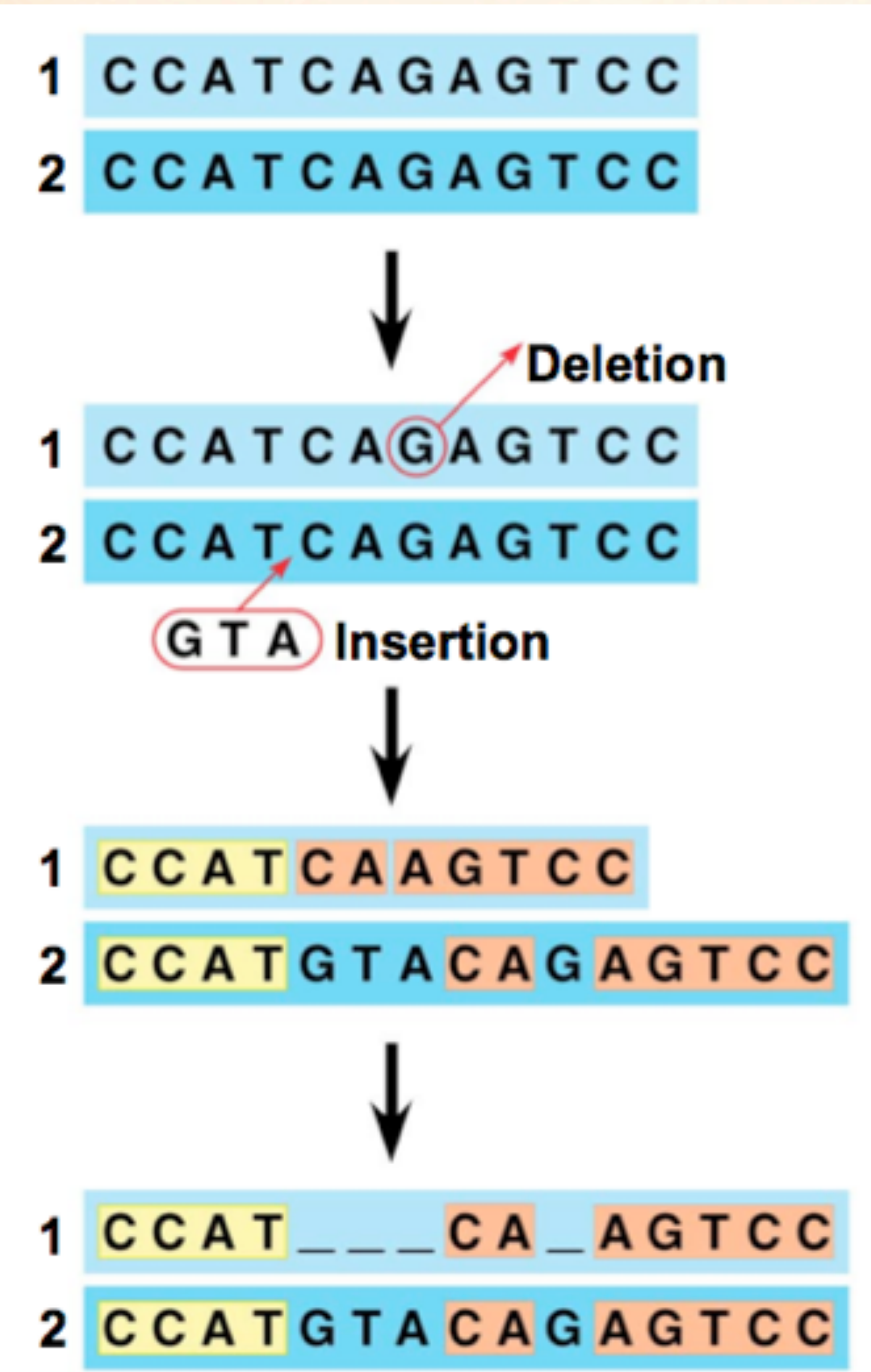


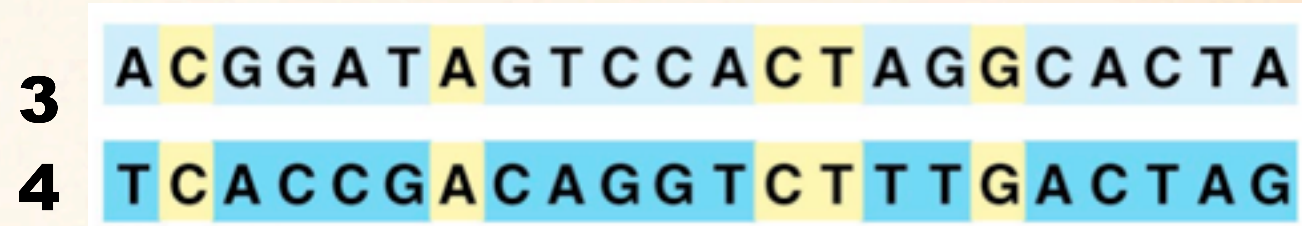


Which set of species are more closely related 1&2 or 3&4?

Species 1 Species 2

Species 3 Species 4

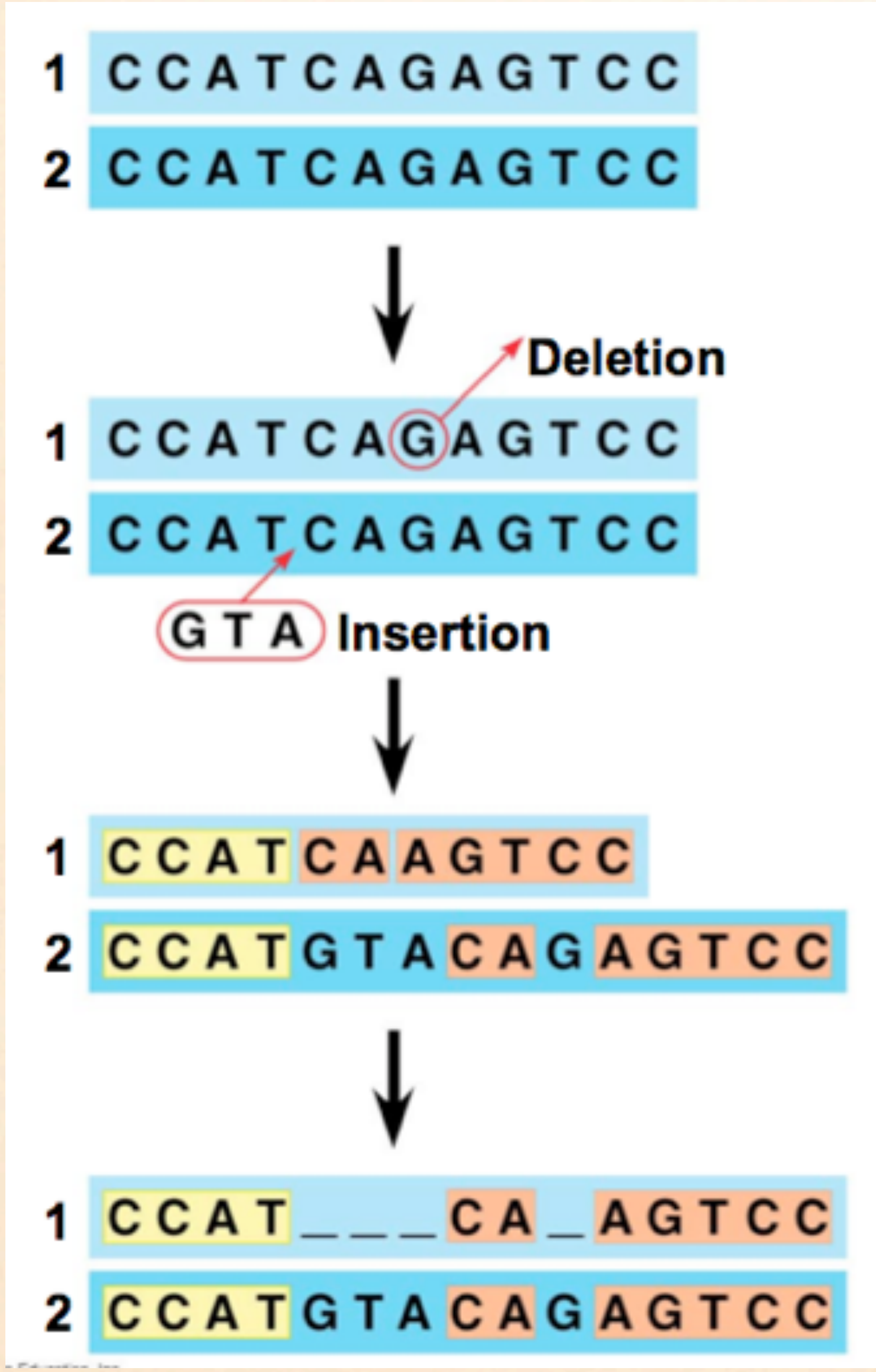




Which set of species are more closely related 1&2 or 3&4?

Species 1&2 are more closely related than 3&4

Turns out that the question on the last slide is very tricky and in reality systematists would rely on the help the of statistical tools and computers to draw the following...



Looking at the third image on the left one would likely conclude these species are very different due to many differences in their sequence, but the computer has determined that they actually share 11/13 bases and are therefore very similar

Turns out that the question on the last slide is very tricky and in reality systematists would rely on the help the of statistical tools and computers to draw the following...

Molecular Homoplasy

3 A C G G A T A G T C C A C T A G G C A C T A

4 T C A C C G A C A G G T C T T T G A C T A G

Looking at the data above one would likely conclude these species are more similar than they are.

The similarities here are actually due to coincidence alone

Maximum Parsimony & Maximum Likelihood

- A growing database of gene sequences allows systematists to better develop phylogenies however the wealth of data are also makes it more difficult.
- In studying just 50 species there are 3×10^{76} different ways to arrange the trees, Which of these trees is the correct one?
- Science can never know for certain, but they can get close by narrowing the possibilities by applying the principles of maximum parsimony and maximum likelihood.

Maximum Parsimony

- The principle of **maximum parsimony**, states that one should first investigate the simplest explanation that is consistent with the facts, also called "Occam's Razor"
    - William Occam was a 14th century English philosopher who advocated this minimalist problem solving technique
    - If you build a tree use morphological data, the most parsimonious tree requires the fewest evolutionary events.
    - If you build a tree use genetic data, the most parsimonious tree requires the fewest base changes.

Maximum Likelihood

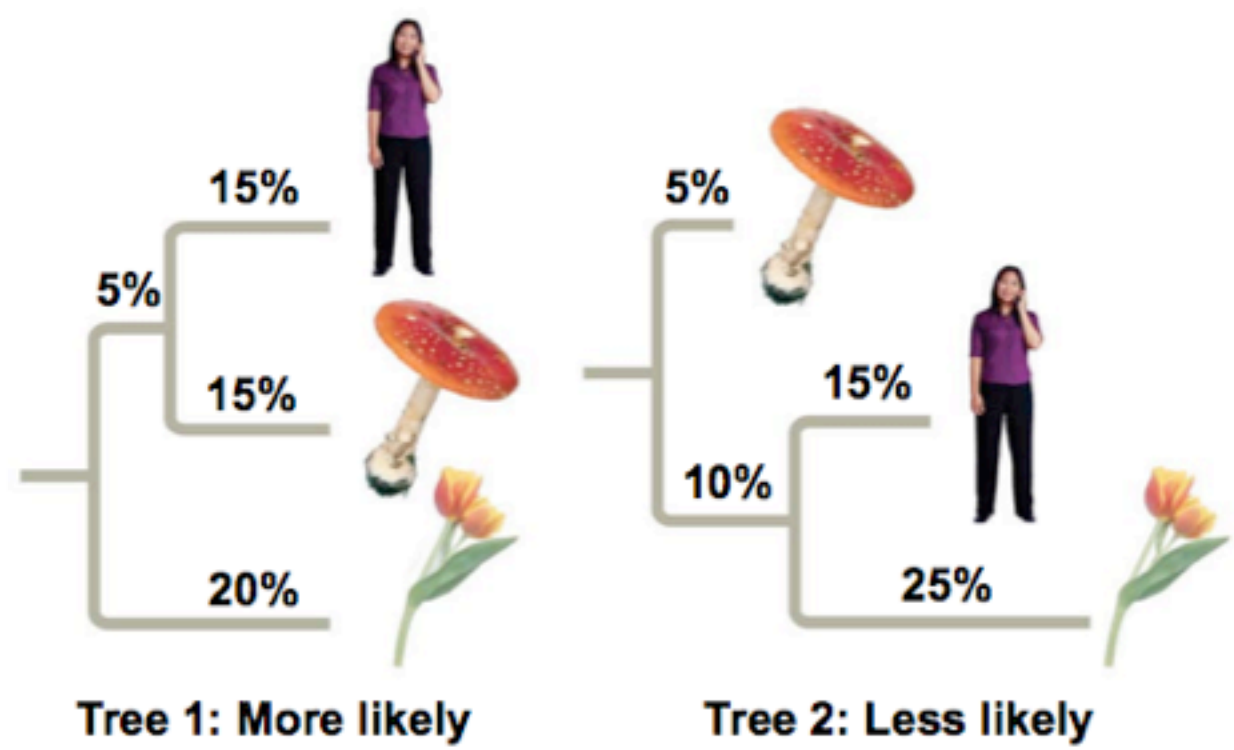
- The principle of **maximum likelihood**, states that given certain probability rules about how DNA sequences change over time, a tree can be found that reflects the most likely sequence of evolutionary events.
- Maximum likelihood methods can get complex, not suprisingly computers can help crunch data in the most likely and parsimonious ways.
- The next slides offer insight into a simple case where we might illustrate these methods.

Maximum Likelihood

Assuming that changes in DNA occur at the same rate tree 1 is more likely, for tree 2 to be right the rate of evolution in the mushroom lineage would have to slow while the rate in the tulip lineage would have to speed up

	Human	Mushroom	Tulip
Human	0	30%	40%
Mushroom		0	40%
Tulip			0

(a) Percentage differences between sequences



(b) Comparison of possible trees

Learning Objectives

LO 1.9 The student is able to evaluate evidence provided by data from many scientific disciplines that support biological evolution. [See **SP 5.3**]

LO 1.10 The student is able to refine evidence based on data from many scientific disciplines that support biological evolution. [See **SP 5.2**]

LO 1.11 The student is able to design a plan to answer scientific questions regarding how organisms have changed over time using information from morphology, biochemistry and geology. [See **SP 4.2**]

LO 1.12 The student is able to connect scientific evidence from many scientific disciplines to support the modern concept of evolution. [See **SP 7.1**]

LO 1.13 The student is able to construct and/or justify mathematical models, diagrams or simulations tha